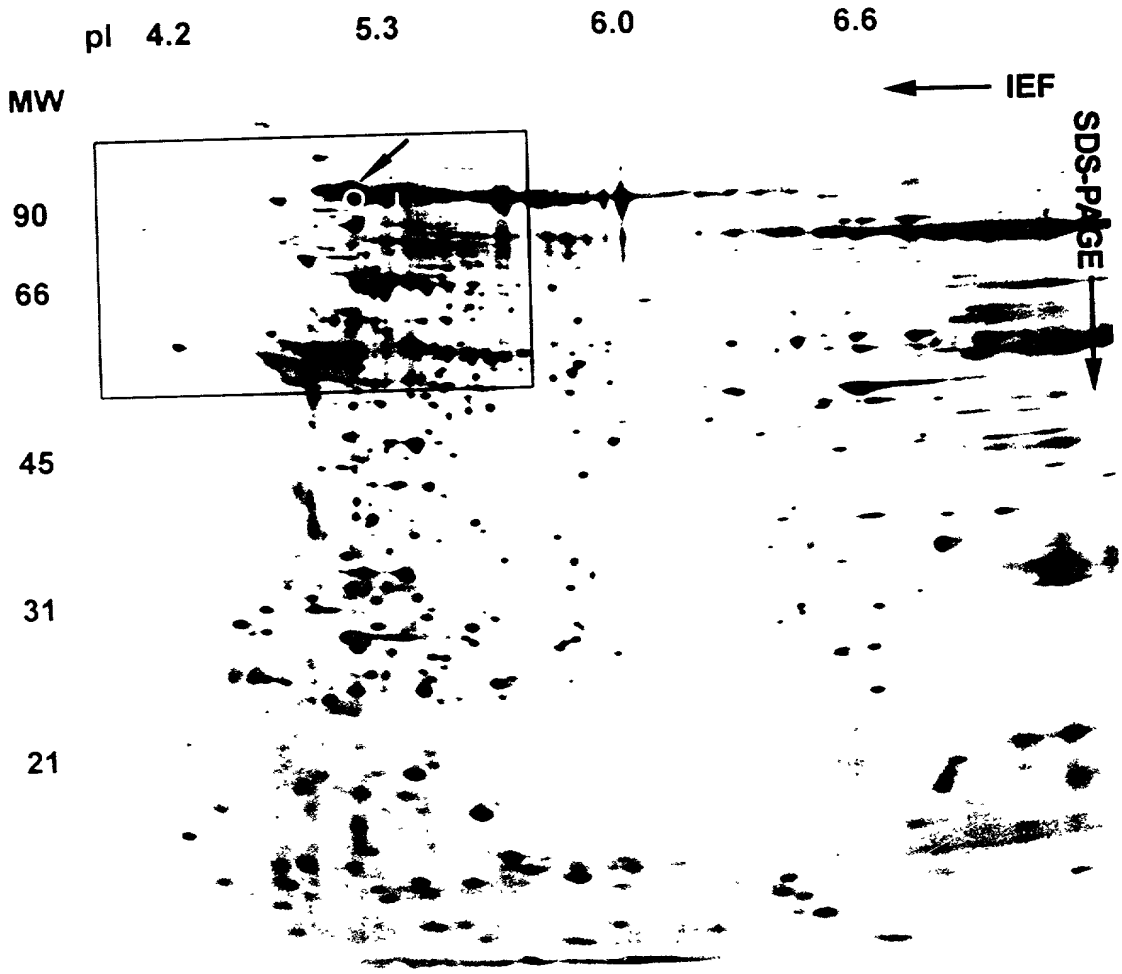

FIG.1A

FIG.1B FIG.1C FIG.1D

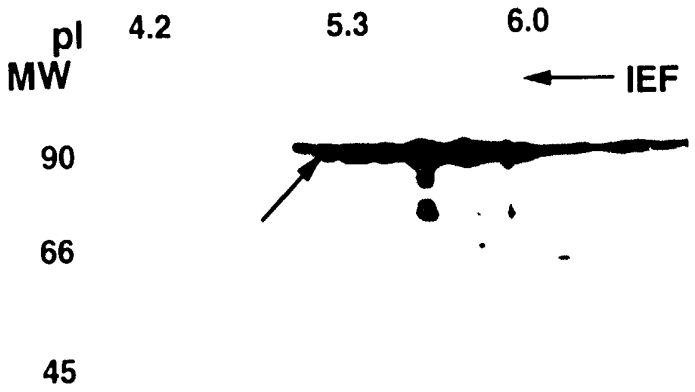

FIG.2A

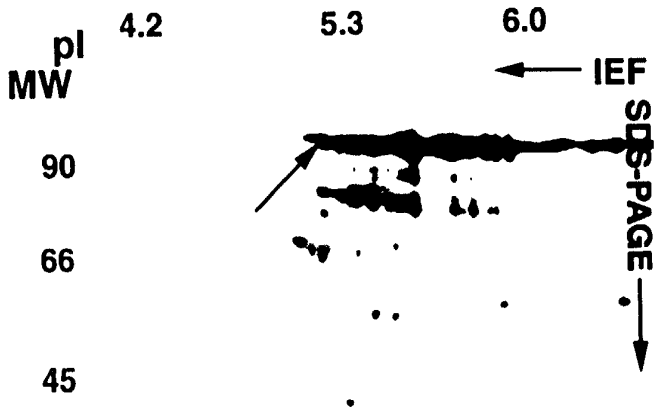

FIG.2B

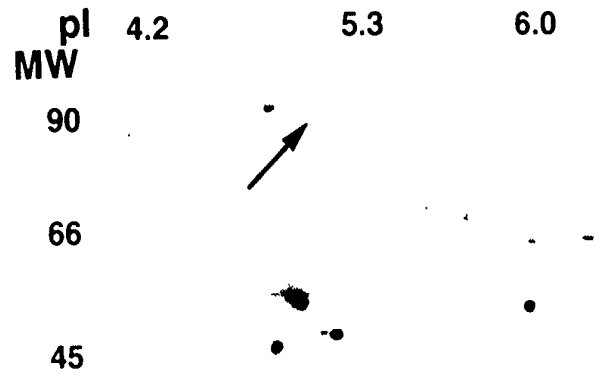

FIG.2C

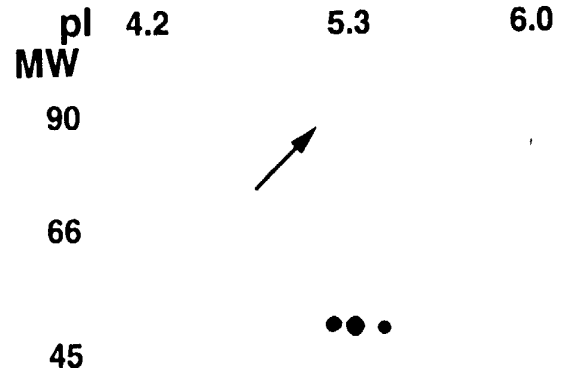

FIG.2D

```
   1 GACTTTAAAAGTATATTCTGGAGTCTTCCGTGGTTCACTATTCCAGTACTACAGAGATTC
  61 CTTATATTACATGGCAGGAGGGGGATAAACTGAGGGATAGTGAAGACAACAATAAATTAA
 121 TCAAGAGCTTTCCTCATATCTCAGAACCTATCCTCTGTAAGAATGTCAGAAAAGGTTGAC
                                                 M  S  E  K  V  D   6
 181 TGGTTACAAAGCCAAAATGGAGTATGCAAAGTTGATGTCTATTCTCCTGGAGACAACCAA
     W  L  Q  S  Q  N  G  V  C  K  V  D  V  Y  S  P  G  D  N  Q  26
 241 GCCCAGGACTGGAAAATGGACACCTCCACGGATCCTGTCAGAGTGCTCAGCTGGCTCCGC
     A  Q  D  W  K  M  D  T  S  T  D  P  V  R  V  L  S  W  L  R  46
 301 AGAGACCTGGAGAAGAGTACAGCAGAGTTCCAAGATGTTCGGTTCAAACCCGGAGAATCA
     R  D  L  E  K  S  T  A  E  F  Q  D  V  R  F  K  P  G  E  S  66
 361 TTTGGTGGGGAAACGTCCAACTCAGGAGACCCACACAAAGGTTTCTCTGTAGACTATTAC
     F  G  G  E  T  S  N  S  G  D  P  H  K  G  F  S  V  D  Y  Y  86
 421 AACACCACCACCAAGGGCACTCCAGAAAGATTGCATTTTGAGATGACTCACAAAGAGATT
     N  T  T  T  K  G  T  P  E  R  L  H  F  E  M  T  H  K  E  I  106
 481 CCTTGCCAGGGCCCCAGGGCCCAACTTGGCAACGGGAGTTCAGTAGATGAAGTTTCCTTC
     P  C  Q  G  P  R  A  Q  L  G  N  G  S  S  V  D  E  V  S  F  126
 541 TATGCTAACCGCCTCACGAATCTAGTCATAGCCATGGCCCGCAAAGAGATCAATGAGAAG
     Y  A  N  R  L  T  N  L  V  I  A  M  A  R  K  E  I  N  E  K  146
 601 ATCGATGGCTCTGAAAACAAATGTGTCTATCAGTCATTGTACATGGGGAATGAACCCACA
     I  D  G  S  E  N  K  C  V  Y  Q  S  L  Y  M  G  N  E  P  T  166
 661 CCCACCAAAAGCCTCAGTAAGATAGCATCAGAGCTTGTGAATGAGACCGTCTCTGCATGT
     P  T  K  S  L  S  K  I  A  S  E  L  V  N  E  T  V  S  A  C  186
 721 TCCAGGAATGCTGCCCCAGACAAGGCTCCTGGCTCTGGAGACAGAGTCTCGGGATCATCA
     S  R  N  A  A  P  D  K  A  P  G  S  G  D  R  V  S  G  S  S  206
 781 CAAAGTCCCCCAAATTTGAAATACAAGTCCACTTTGAAGATCAAGGAGAGCACCAAAGAA
     Q  S  P  P  N  L  K  Y  K  S  T  L  K  I  K  E  S  T  K  E  226
 841 AGACAGGGTCCAGATGACAAGCCTCCTTCTAAGAAGTCTTTCTTCTATAAGGAAGTGTTT
     R  Q  G  P  D  D  K  P  P  S  K  K  S  F  F  Y  K  E  V  F  246
 901 GAATCTCGTAACGGAGATTATGCCAGAGAGGGTGGAAGGTTCTTTCCTCGGGAGAGAAAG
     E  S  R  N  G  D  Y  A  R  E  G  G  R  F  F  P  R  E  R  K  266
 961 AGGTTTCGAGGGCAGGAAAGGCCTGATGACTTTACGGCTTCTGTTGGTGAAGGGATCATG
     R  F  R  G  Q  E  R  P  D  D  F  T  A  S  V  G  E  G  I  M  286
1021 ACCTATGCTAACAGTGTGGTATCTGATATGATGGTCTCCATCATGAAGACACTGAAGATC
     T  Y  A  N  S  V  V  S  D  M  M  V  S  I  M  K  T  L  K  I  306
1081 CAAGTGAAAGACACAACCATTGCCACCATCCTACTGAAGAAGGTTCTGCTCAAGCATGCA
     Q  V  K  D  T  T  I  A  T  I  L  L  K  K  V  L  L  K  H  A  326
```

FIG.3A

```
1141 AAAGAGGTGGTCTCGGATCTCATCGACTCCTTCTTGAGGAATCTCCACAGCGTCACAGGG
     K  E  V  V  S  D  L  I  D  S  F  L  R  N  L  H  S  V  T  G   346
1201 ACCCTCATGACTGACACACAGTTTGTCTCGGCTGTGAAAAGAACTGTCTTCTCTCATGGA
     T  L  M  T  D  T  Q  F  V  S  A  V  K  R  T  V  F  S  H  G   366
1261 AGCCAAAAGGCCACAGATATCATGGATGCCATGCTAAGGAAGCTGTACAATGTAATGTTT
     S  Q  K  A  T  D  I  M  D  A  M  L  R  K  L  Y  N  V  M  F   386
1321 GCCAAGAAAGTCCCTGAGCATGTCAGGAAAGCCCAAGACAAGGCTGTGAGTTATTCCCTC
     A  K  K  V  P  E  H  V  R  K  A  Q  D  K  A  V  S  Y  S  L   406
1381 ATCTCCATGAAAGGAATGGGTGATCCTAAAAACCGAAATGTGAACTTTGCCATGAAATCT
     I  S  M  K  G  M  G  D  P  K  N  R  N  V  N  F  A  M  K  S   426
1441 GAAACTAAATTGAGAGAAAAAATGTATTCTGAACCCAAATCAGAGGAGGAGACTTGTGCG
     E  T  K  L  R  E  K  M  Y  S  E  P  K  S  E  E  E  T  C  A   446
1501 AAAACTCTGGGTGAGCACATTATCAAAGAGGGGCTTACCCTGTGGCATAAAAGTCAGCAG
     K  T  L  G  E  H  I  I  K  E  G  L  T  L  W  H  K  S  Q  Q   466
1561 AACGAATGTAAATCTCTAGGTTTCCAGCATGCAGCATTCGAAGCTCCCAACACACAGCGT
     N  E  C  K  S  L  G  F  Q  H  A  A  F  E  A  P  N  T  Q  R   486
1621 AAGCCTGCATCAGACATTTCCTTTGAGTACCCTGAAGATACTGGCAACCTCAGCCTTCCT
     K  P  A  S  D  I  S  F  E  Y  P  E  D  T  G  N  L  S  L  P   506
1681 CCATATCCTCCAGAGAAACCTGAGAATTTTATGTATGATTCAGACTCCTGGGCCAAGGAC
     P  Y  P  P  E  K  P  E  N  F  M  Y  D  S  D  S  W  A  K  D   526
1741 CTGATCGTGTCTGCCCTGCTTCTGATTCAATATCACCTGGCCCAGGGAGGAAGAAGGGAT
     L  I  V  S  A  L  L  L  I  Q  Y  H  L  A  Q  G  G  R  R  D   546
1801 GCACGGAGCTTCGTTGAAGCTGCTGGCACCACCAACTTTCCTGCCAATGAACCTCCTGTA
     A  R  S  F  V  E  A  A  G  T  T  N  F  P  A  N  E  P  P  V   566
1861 GCTCCCGATGAATCTTGCCTTAAGTCTGCTCCCATTGTAGGTGACCAAGAACAAGCAGAA
     A  P  D  E  S  C  L  K  S  A  P  I  V  G  D  Q  E  Q  A  E   586
1921 AAGAAGGACCTAAGGAGTGTTTTCTTTAATTCCATCCGGAACTTACTTAGTGAGACCATT
     K  K  D  L  R  S  V  F  F  N  S  I  R  N  L  L  S  E  T  I   606
1981 TTCAAGCGTGACCAGAGCCCTGAACCCAAGGTGCCGGAACAGCCAGTTAAGGAAGATAGG
     F  K  R  D  Q  S  P  E  P  K  V  P  E  Q  P  V  K  E  D  R   626
2041 AAGTTGTGTGAAAGACCGTTGGCGTCTTCTCCCCCCAGGCTATATGAGGATGATGAGACC
     K  L  C  E  R  P  L  A  S  S  P  P  R  L  Y  E  D  D  E  T   646
2101 CCTGGTGCCCTTTCTGGGCTGACCAAGATGGCTGTCAGCCAGATAGATGGCCACATGAGT
     P  G  A  L  S  G  L  T  K  M  A  V  S  Q  I  D  G  H  M  S   666
2161 GGGCAGATGGTAGAACATCTGATGAACTCAGTGATGAAGCTGTGTGTCATCATTGCTAAG
     G  Q  M  V  E  H  L  M  N  S  V  M  K  L  C  V  I  I  A  K   686
```

FIG.3B

```
2221 TCCTGTGATGCTTCGTTGGCAGAGCTGGGAGATGACAAGCTGGGAGATGCCAGTAGGCTA
     S C D A S L A E L G D D K L G D A S R L  706
2281 ACTTCGGCCTTCCCAGATAGTTTATATGAGTGCTTACCAGCCAAGGGCACAGGGTCAGCA
     T S A F P D S L Y E C L P A K G T G S A  726
2341 GAAGCTGTCCTGCAGAATGCCTATCAAGCTATCCATAACGAAATGAGAGGCACATCAGGA
     E A V L Q N A Y Q A I H N E M R G T S G  746
2401 CAGCCCCCTGAAGGGTGTGCAGCACCCACGGTGATTGTCAGCAATCACAACCTAACGGAC
     Q P P E G C A A P T V I V S N H N L T D  766
2461 ACAGTTCAGAACAAGCAACTCCAAGCCGTCCTTCAATGGGTAGCTGCCTCTGAGCTCAAT
     T V Q N K Q L Q A V L Q W V A A S E L N  786
2521 GTCCCTATTTTGTATTTTGCTGGTGATGATGAAGGGATCCAGGAGAAGCTACTTCAGCTC
     V P I L Y F A G D D E G I Q E K L L Q L  806
2581 TCAGCTGCTGCTGTGGACAAAGGATGCAGTGTGGGCGAGGTTCTGCAGTCGGTGCTGCGC
     S A A A V D K G C S V G E V L Q S V L R  826
2641 TATGAGAAGGAGCGCCAGCTGAATGAGGCGGTGGGGAATGTCACACCGCTGCAGCTGCTG
     Y E K E R Q L N E A V G N V T P L Q L L  846
2701 GACTGGCTGATGGTGAACCTGTAATCGGCAACCCCACTGCTTTCCCCTCTTCTGGCAGTG
     D W L M V N L *                        853
2761 GGGCCGGCCCTTATCCCCGCCCTTCTTTCTCACTTCCACATCTCCCCCTCTATATCCTCA
2821 CAGAGCCCTAACATTATCTTCACACCACTCTCATCAAAGACATGTCATCTTGTGCTAGCC
2881 ACTGGATTTTGCAGATTTTCCTGTCCGTGCAAGCAAGGACGTAAAATTAAAAAATTACAA
2941 TG
```

FIG.3C

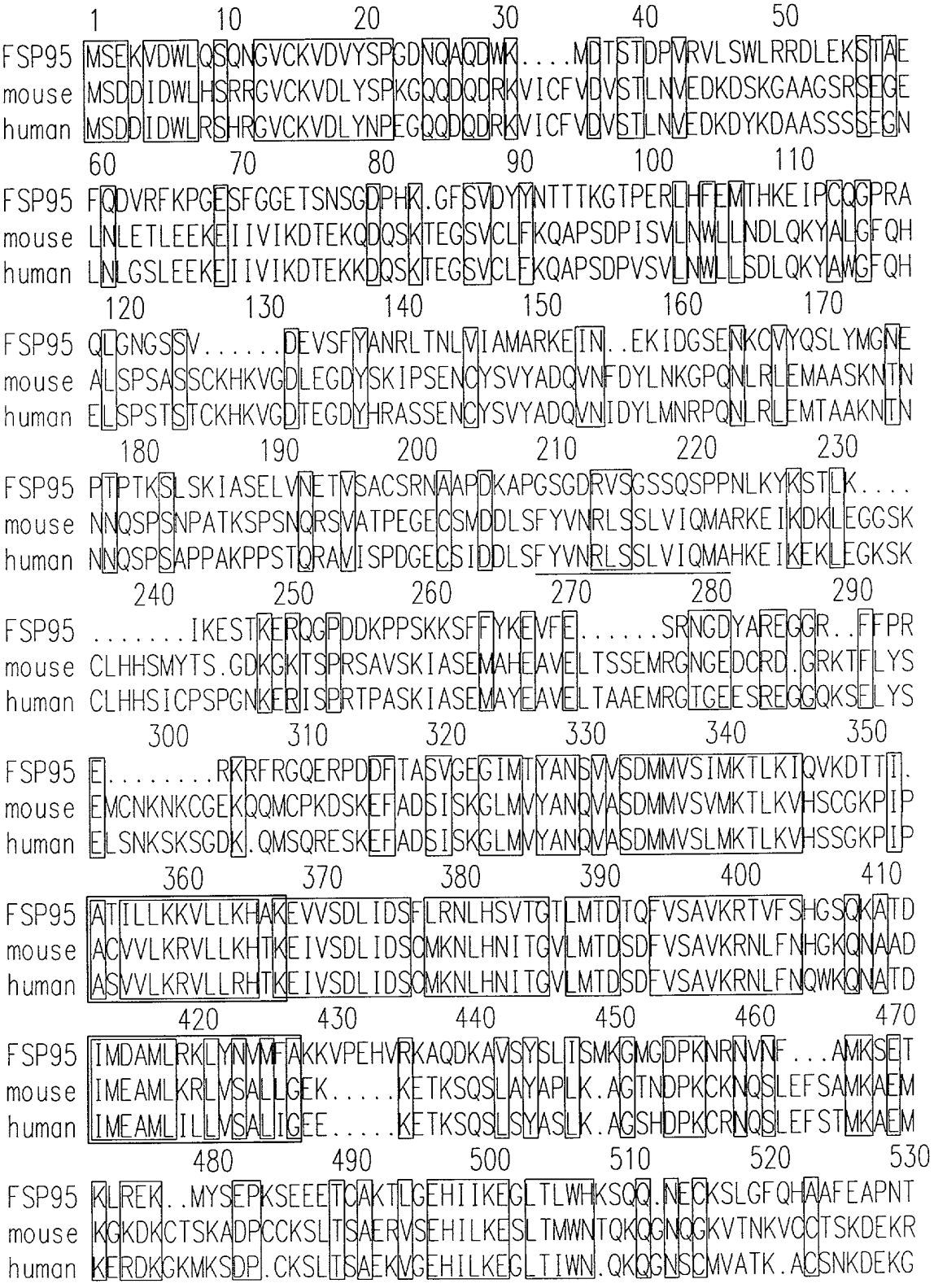
1 10 20 30 40 50
FSP95 MSEKVDWLQSQNGVCKVDVYSPGDNQAQDWK....MDTSTDPVRVLSWLRRDLEKSTAE
mouse MSDDIDWLHSRRGVCKVDLYSPKGQQDQDRKVICFVDVSTLNVEDKDSKGAAGSRSEGE
human MSDDIDWLRSHRGVCKVDLYNPEGQQDQDRKVICFVDVSTLNVEDKDYKDAASSSSEGN
60 70 80 90 100 110
FSP95 FQDVRFKPGESFGGETSNSGDPHK.GFSVDYYNTTTKGTPERLHFEMTHKEIPCQGPRA
mouse LNLETLEEKEIIVIKDTEKQDQSKTEGSVCLFKQAPSDPISVLNWLLNDLQKYALGFQH
human LNLGSLEEKEIIVIKDTEKKDQSKTEGSVCLFKQAPSDPVSVLNWLLSDLQKYAWGFQH
120 130 140 150 160 170
FSP95 QLGNGSSV.....DEVSFYANRLTNLVIAMARKEIN..EKIDGSENKCVYQSLYMGNE
mouse ALSPSASSCKHKVGDLEGDYSKIPSENCYSVYADQVNFDYLNKGPQNLRLEMAASKNTN
human ELSPSTSTCKHKVGDTEGDYHRASSENCYSVYADQVNIDYLMNRPQNLRLEMTAAKNTN
180 190 200 210 220 230
FSP95 PTPTKSLSKIASELVNETVSACSRNAAPDKAPGSGDRVSGSSQSPPNLKYKSTLK....
mouse NNQSPSNPATKSPSNQRSVATPEGECSMDDLSFYVNRLSSLVIQMARKEIKDKLEGGSK
human NNQSPSAPPAKPPSTQRAVISPDGECSIDDLSFYVNRLSSLVIQMAHKEIKEKLEGKSK
240 250 260 270 280 290
FSP95 .....IKESTKERQGPDDKPPSKKSFFYKEVFE.....SRNGDYAREGGR..FFPR
mouse CLHHSMYTS.GDKGKTSPRSAVSKIASEMAHEAVELTSSEMRGNGEDCRD.GRKTFLYS
human CLHHSICPSPGNKERISPRTPASKIASEMAYEAVELTAAEMRGTGEESREGGQKSELYS
300 310 320 330 340 350
FSP95 E.....RKRFRGQERPDDFTASVGEGIMTYANSVVSDMMVSIMKTLKTQVKDTTI.
mouse EMCNKNKCGEKQQMCPKDSKEFADSISKGLMVYANQVASDMMVSVMKTLKVHSCGKPIP
human ELSNKSKSGDK.QMSQRESKEFADSISKGLMVYANQVASDMMVSLMKTLKVHSSGKPIP
360 370 380 390 400 410
FSP95 ATILLKKVLLKHAKEVVSDLIDSFLRNLHSVTGTLMTDTQFVSAVKRTVFSHGSQKATD
mouse ACVVLKRVLLKHTKEIVSDLIDSQMKNLHNITGVLMTDSDFVSAVKRNLFNHGKQNAAD
human ASVVLKRVLLRHTKEIVSDLIDSQMKNLHNITGVLMTDSDFVSAVKRNLFNQWKQNATD
420 430 440 450 460 470
FSP95 IMDAMLRKLYNVMFAKKVPEHVRKAQDKAVSYSLISMKGMGDPKNRNVNF...AMKSET
mouse IMEAMLKRLVSALLGEK.....KETKSQSLAYAPLK.AGTNDPKCKNQSLEFSAMKAEM
human IMEAMLILLVSALIGEE.....KETKSQSLSYASLK.AGSHDPKCRNQSLEFSTMKAEM
480 490 500 510 520 530
FSP95 KLREK..MYSEPKSEEETCAKTLGEHIIKEGLTLWHKSQQ.NECKSLGFQHAAFEAPNT
mouse KGKDKCTSKADPCCKSLTSAERVSEHILKESLTMWNTQKQGNQGKVTNKVCCTSKDEKR
human KERDKGKMKSDP.CKSLTSAEKVGEHILKEGLTIWN.QKQGNSCMVATK.ACSNKDEKG

FIG.4A

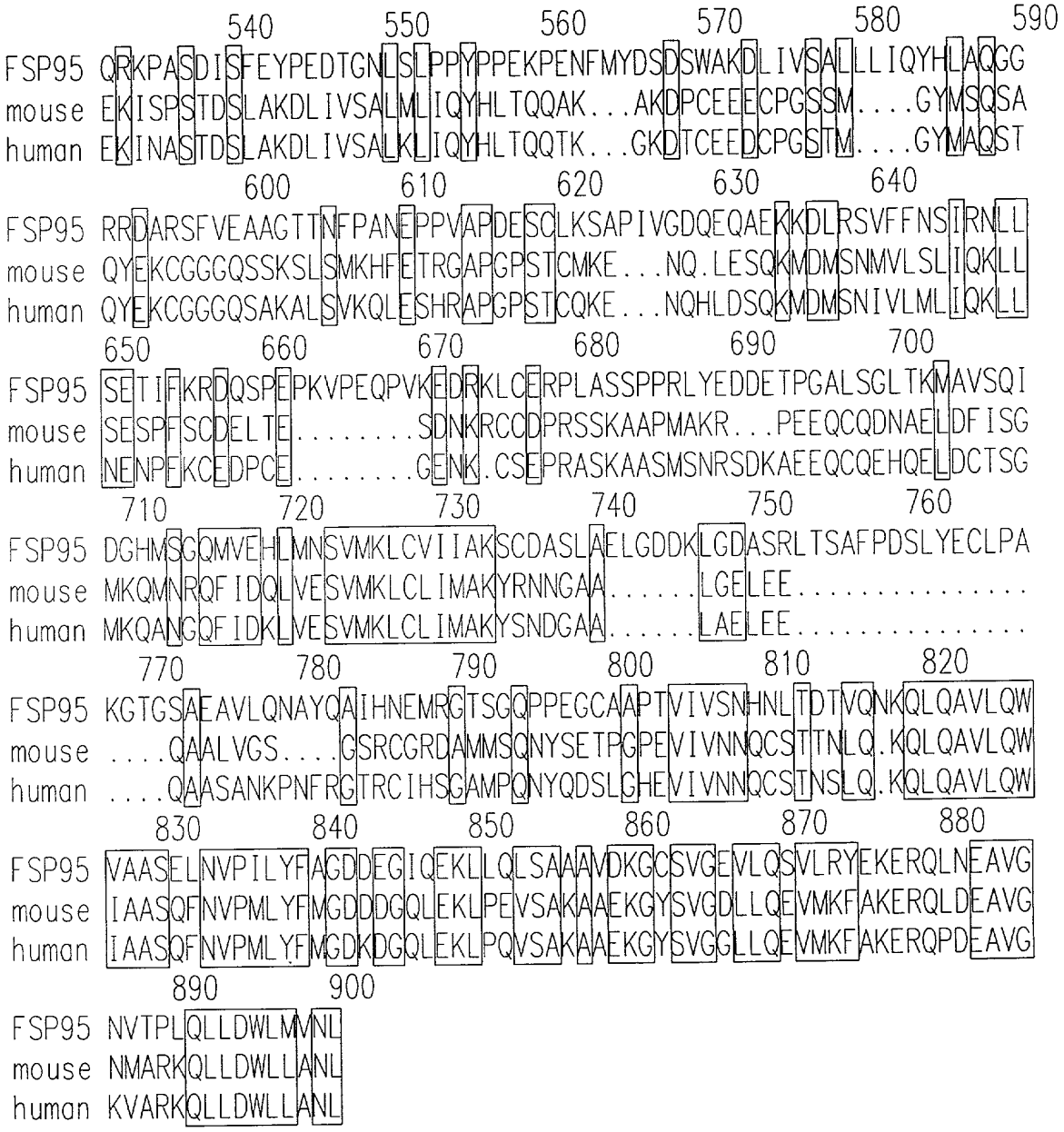
540 550 560 570 580 590
FSP95 QRKPASDISFEYPEDTGNLSLPPYPPEKPENFMYDSDSWAKDLIVSALLLIQYHLAQGG
mouse EKISPSTDSLAKDLIVSALMLIQYHLTQQAK...AKDPCEEECPGSSM....GYMSQSA
human EKINASTDSLAKDLIVSALKLIQYHLTQQTK...GKDTCEEDCPGSTM....GYMAQST
600 610 620 630 640
FSP95 RRDARSFVEAAGTTNFPANEPPVAPDESCLKSAPIVGDQEQAEKKDLRSVFFNSIRNLL
mouse QYEKCGGGQSSKSLSMKHFETRGAPGPSTCMKE...NQ.LESQKMDMSNMVLSLIQKLL
human QYEKCGGGQSAKALSVKQLESHRAPGPSTCQKE...NQHLDSQKMDMSNIVLMLIQKLL
650 660 670 680 690 700
FSP95 SETIFKRDQSPEPKVPEQPVKEDRKLCERPLASSPPRLYEDDETPGALSGLTKMAVSQI
mouse SESPFSCDELTE.....SDNKRCCDPRSSKAAPMAKR...PEEQCQDNAELDFISG
human NENPFKCEDPCE.....GENK.CSEPRASKAASMSNRSDKAEEQCQEHQELDCTSG
710 720 730 740 750 760
FSP95 DGHMSGQMVEHLMNSVMKLCVIIAKSCDASLAELGDDKLGDASRLTSAFPDSLYECLPA
mouse MKQMNRQFIDQLVESVMKLCLIMAKYRNNGAA.....LGELEE.....
human MKQANGQFIDKLVESVMKLCLIMAKYSNDGAA.....LAELEE.....
770 780 790 800 810 820
FSP95 KGTGSAEAVLQNAYQAIHNEMRGTSGQPPEGCAAPTVIVSNHNLTDTVQNKQLQAVLQW
mouse ....QAALVGS....GSRCGRDAMMSQNYSETPGPEVIVNNQCSTTNLQ.KQLQAVLQW
human ....QAASANKPNFRGTRCIHSGAMPQNYQDSLGHEVIVNNQCSTNSLQ.KQLQAVLQW
830 840 850 860 870 880
FSP95 VAASELNVPILYFAGDDEGIQEKLLQLSAAAVDKGCSVGEVLQSVLRYEKERQLNEAVG
mouse IAASQFNVPMLYFMGDDDGQLEKLPEVSAKAAEKGYSVGDLLQEVMKFAKERQLDEAVG
human IAASQFNVPMLYFMGDKDGQLEKLPQVSAKAAEKGYSVGGLLQEVMKFAKERQPDEAVG
890 900
FSP95 NVTPLQLLDWLMVNL
mouse NMARKQLLDWLLANL
human KVARKQLLDWLLANL

FIG.4B

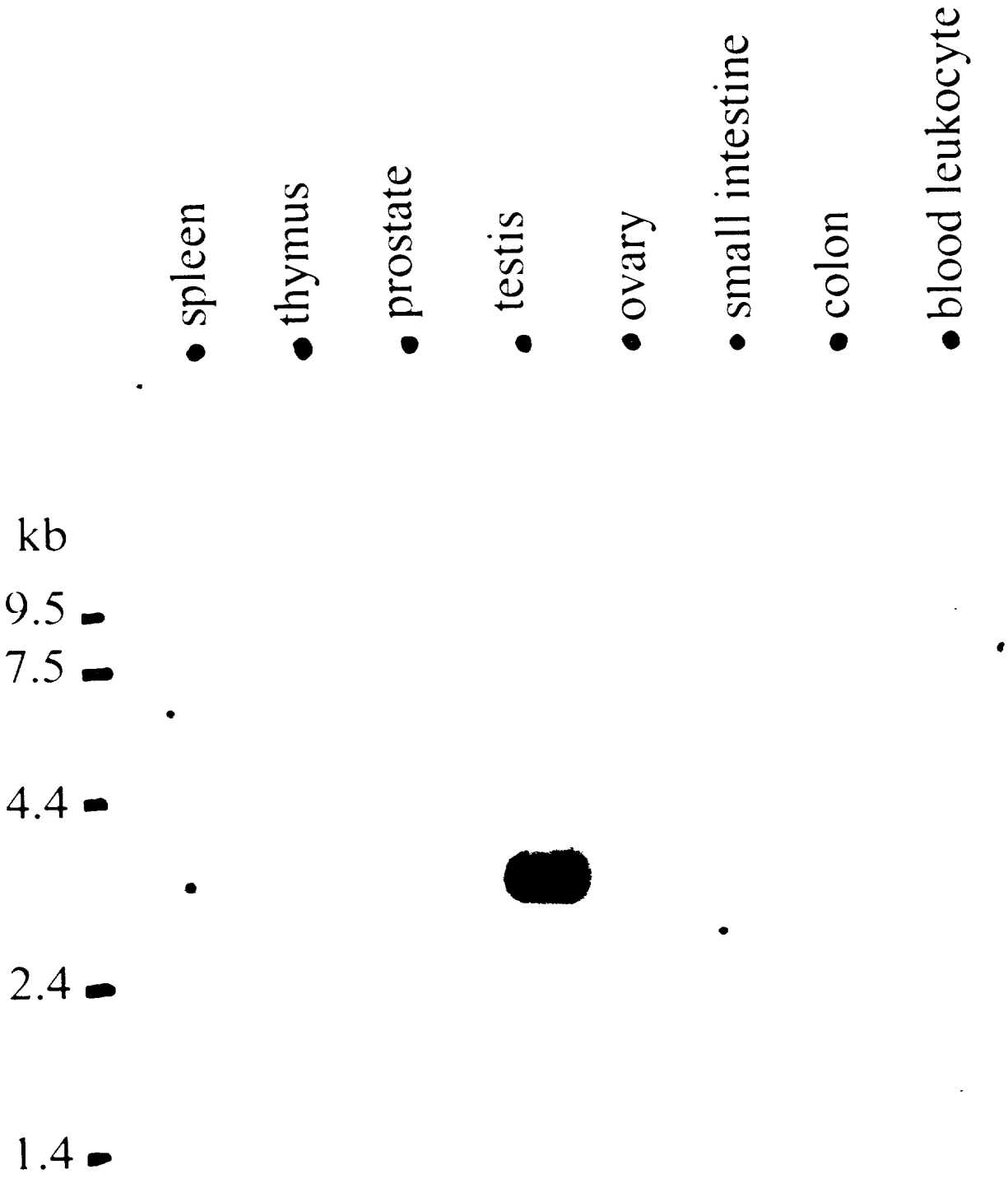
spleen
thymus
prostate
testis
ovary
small intestine
colon
blood leukocyte
kb
9.5
7.5
4.4
2.4
1.4

FIG.5A

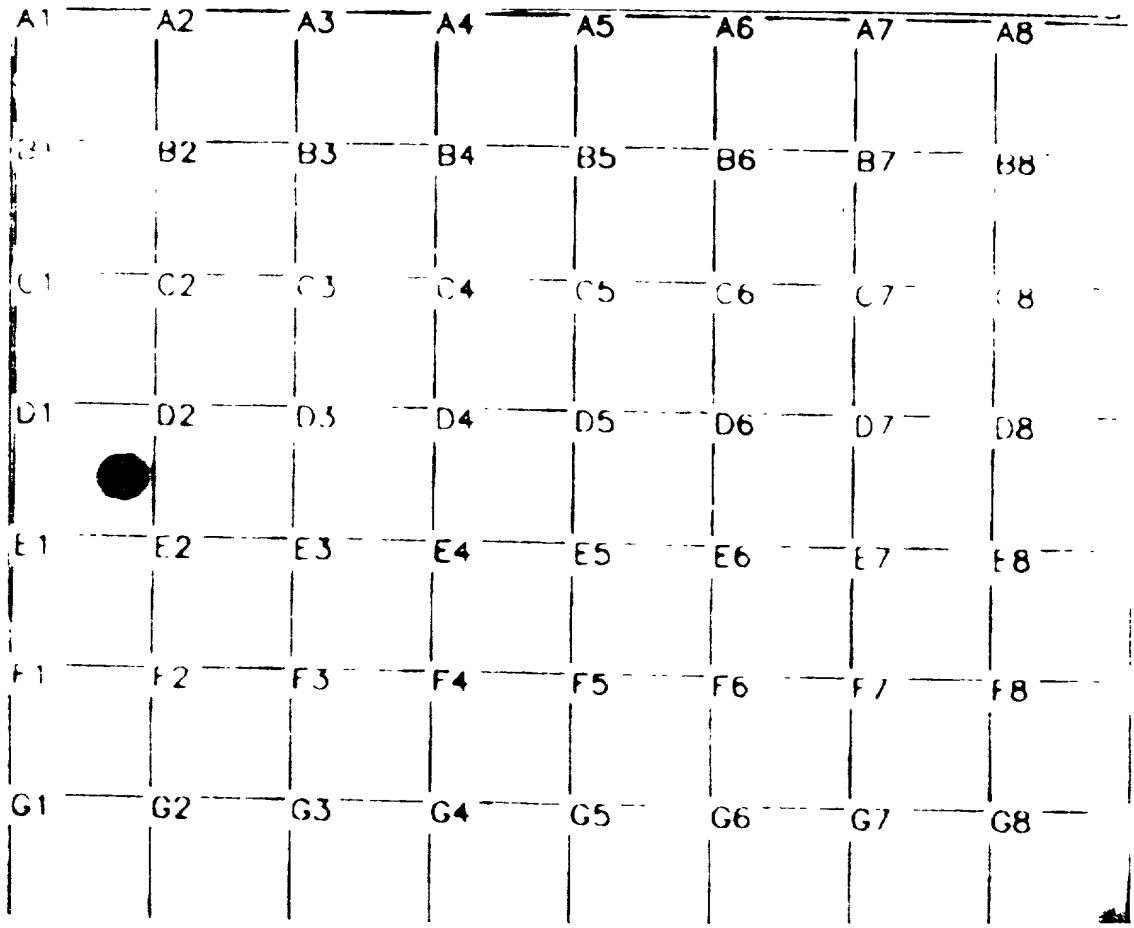
A1
A2
A3
A4
A5
A6
A7
A8
B2
B3
B4
B5
B6
B7
B8
C2
C3
C4
C5
C6
C7
D1
D2
D3
D4
D5
D6
D7
D8
E1
E2
E3
E4
E5
E6
E7
E8
F1
F2
F3
F4
F5
F6
F7
F8
G1
G2
G3
G4
G5
G6
G7
G8

FIG.5B

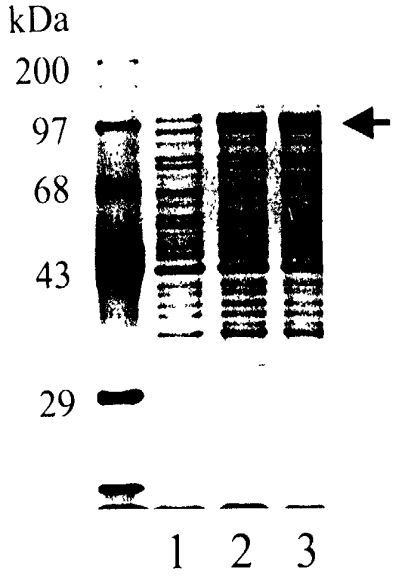

FIG.6A

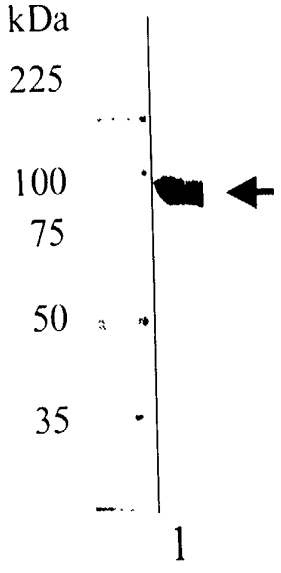

FIG.6B

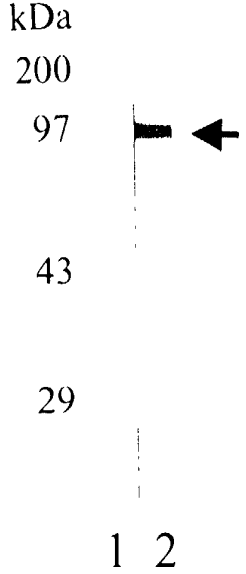

FIG.6C

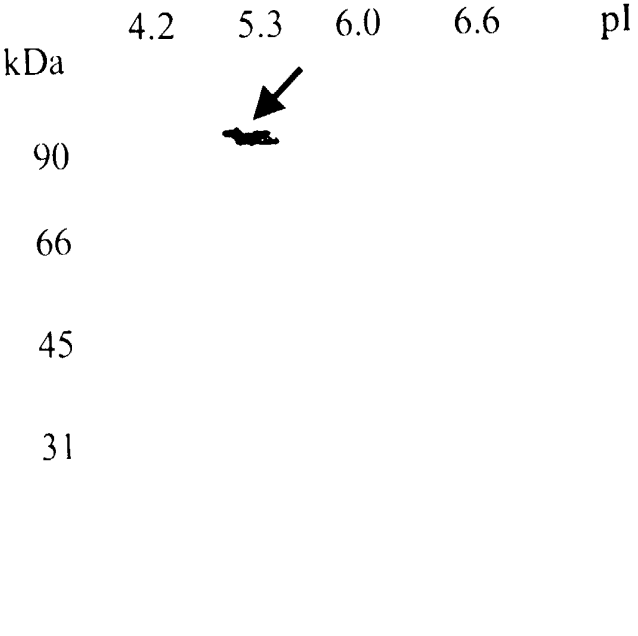

FIG.6D

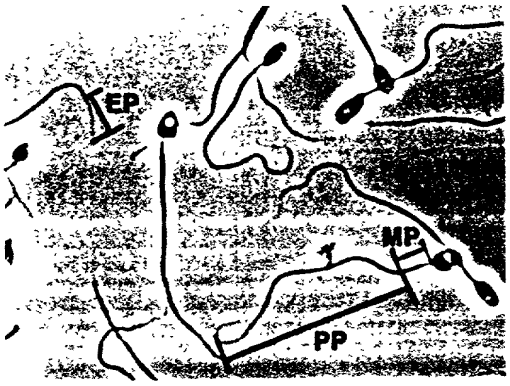

FIG.7A

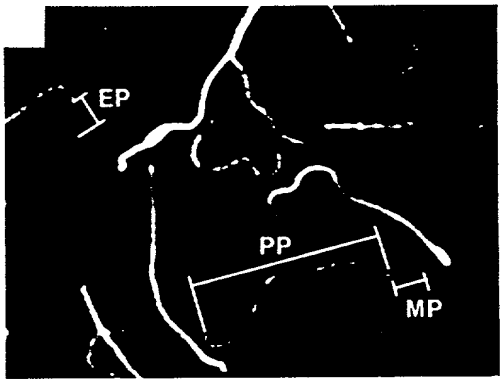

FIG.7B

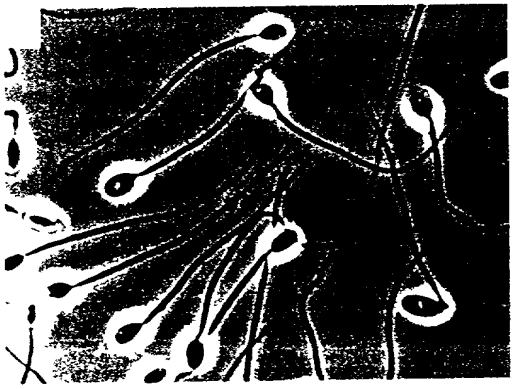

FIG.7C

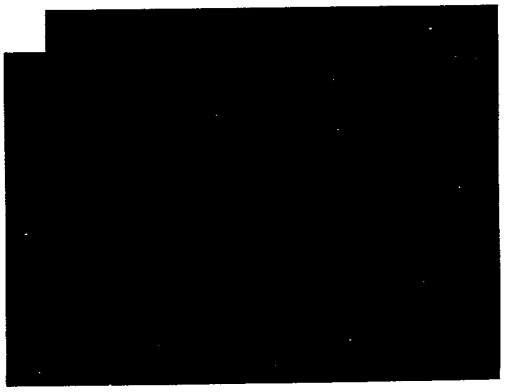

FIG.7D

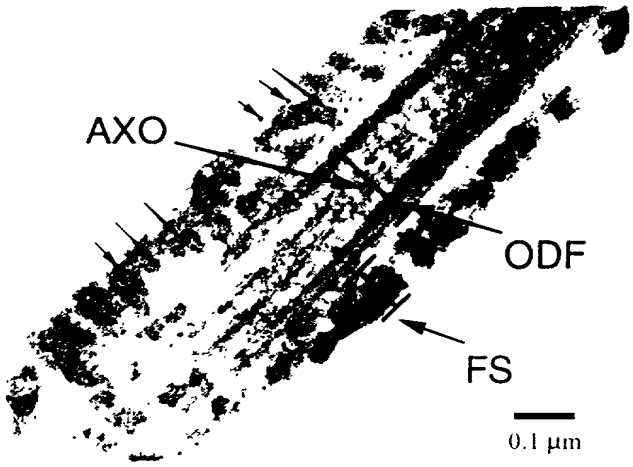

FIG.8A

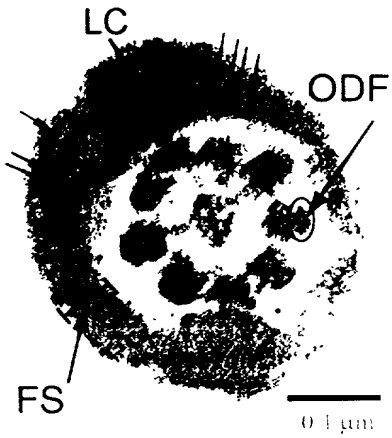

FIG.8B

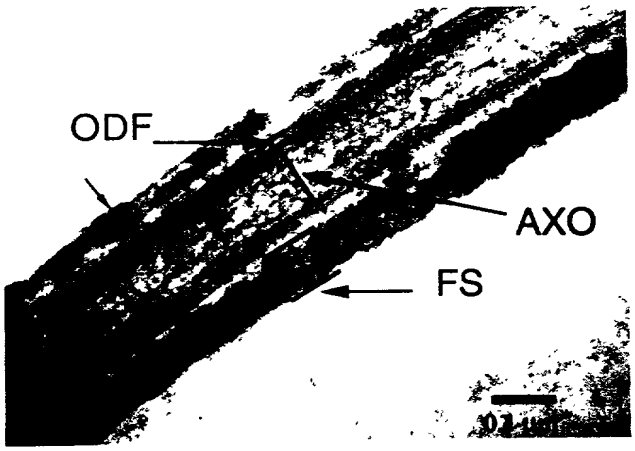

FIG.8C

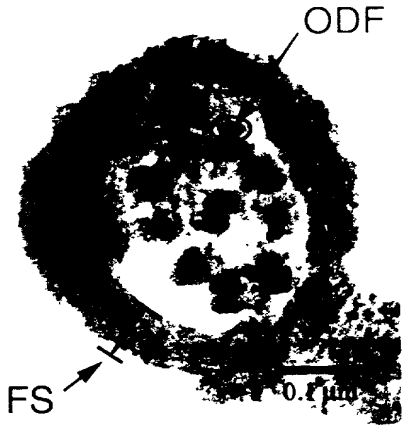

FIG.8D

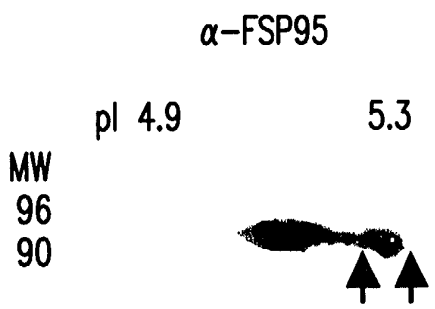

FIG.9A

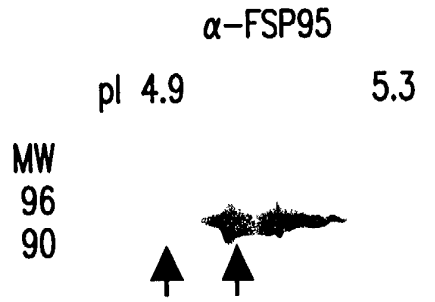

FIG.9B

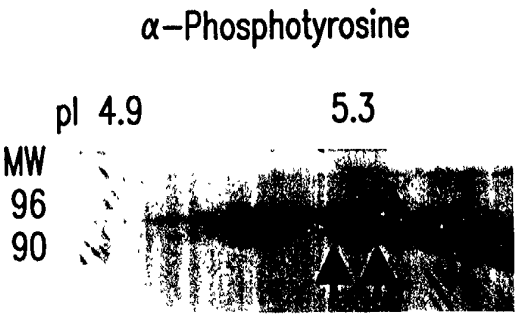

FIG.9C

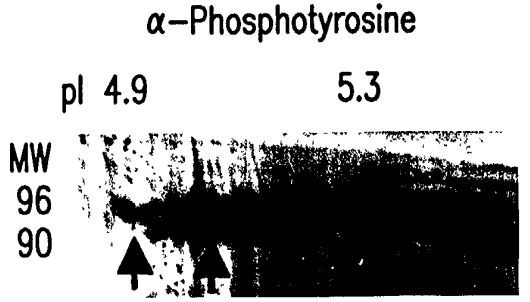

FIG.9D

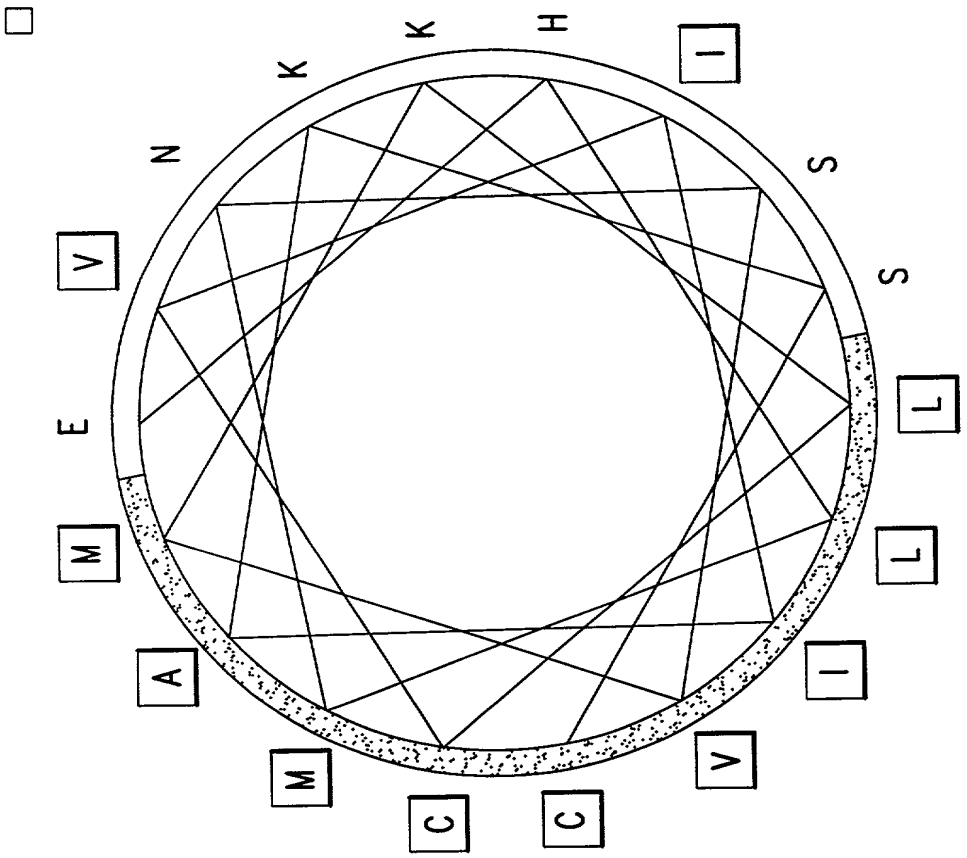

FIG.10